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1: Mol Gen Genet 1998 Feb;257(4):387-91 Related Articles, Books, LinkOut

COP1b, an isoform of COP1 generated by alternative splicing, has a negative effect on COP1 function in regulating light-dependent seedling development in Arabidopsis.

Zhou DX, Kim YJ, Li YF, Carol P, Mache R.

Laboratoire de Genetique Moleculaire des Plantes, Universite Joseph Fourier, Grenoble, France.

COP1 is a negative regulator of Arabidopsis light-dependent development. Mutation of the COP1 locus causes constitutive photomorphogenesis in the dark. Here, we report the identification of an isoform of the COP1 protein, named COP1b, which is generated by alternative splicing. COP1b has a 60-amino acid deletion in the WD-40 repeat domain relative to the full-length COP1. This splicing step is light-independent and takes place mostly in mature seeds and in germinating seedlings. Transgenic Arabidopsis plants that overexpress COP1b show a de-etiolated phenotype in the dark, with a short hypocotyl, open and developed cotyledons. The transgenic seedlings are adult-lethal. These phenotypes closely resemble that of severe cop-1 mutants, indicating that COP1b has a dominant negative effect on COP1 function.

PMID: 9529519 [PubMed - indexed for MEDLINE]

Display Abstract Sort Save Text Clip Add Order

Query: gi|2326943 Xenopus laevis mRNA for Fizzy-related protein, and translated products
Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus

All hits | Common Tree | Taxonomy Report | 3D structures | CDD-Search | GI list

22 BLAST hits to 6 unique species in *Viridiplantae* Sort by taxonomy proximity

0 Archaea | 70 Bacteria | 44 Metazoa | 45 Fungi | 22 Plants | 0 Viruses | 4 Other Eukaryotae

Keep only ▼ Cut-Off 100 Select Reset

493 aa

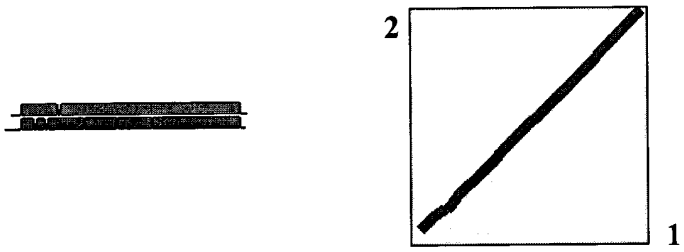
SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
16				
1249	3	AAF37386	7158292	WD-repeat cell cycle regulatory prote
1248	3	AAD22612	4558462	cell cycle switch protein [Medicago s
1240	3	AAM20437	20466239	putative fizzy-related protein [Arab:
1240	3	CAA19806	3292816	putative fizzy-related protein [Arab:
1237	3	AAL36231	17380838	putative Srw1 protein [Arabidopsis th
1				
1215	3	CAB44330	5002527	Srw1-like protein [Arabidopsis thalia
1192	3	BAB11112	10177650	cell cycle switch protein [Arabidops:
1191	3	AAM20433	20466231	cell cycle switch protein [Arabidops:
4				
893	3	BAB63690	15289995	putative cell cycle switch protein [(
2				
882	3	CAB38784	4490293	WD-repeat protein-like protein [Arab:
867	3	CAA11819	3668118	hypothetical protein [Brassica napus]
12				
807	3	NP_198109	15240985	cdc20-like protein [Arabidopsis thal:
1				
791	3	AAB63030	2253631	WD-repeat protein [Daucus carota]
786	3	NP_198060	15240441	putative cdc20 protein [Arabidopsis t
786	3	AAD48933	5732032	contains similarity to Pfam family PI
784	3	NP_198042	15240403	WD-repeat protein - like [Arabidopsis
782	3	AAB61049	2191163	contains similarity to beta transduc:
3				
735	3	AAF14048	6491862	putative cdc20 protein [Arabidopsis t
729	3	CAB38785	4490294	WD-repeat protein-like protein [Arab:
1				
680	3	NP_568505	18421178	WD-repeat protein - like [Arabidopsis
123				

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.1.2 [Oct-19-2000]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 300 wordsize: 3 Filter Align

Sequence 1 gi 7290520 fzr gene product [Drosophila melanogaster] **Length** 478 (1 .. 478)
Sequence 2 gi 10177650 **Length** 472 (1 .. 472)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 457 bits (1164), Expect = e-127
Identities = 237/445 (53%), Positives = 286/445 (64%), Gaps = 18/445 (4%)

```
Query: 23  NNFESSTTPTSLDRFIPCRAYNNWQTNFASINKSNDNSPQTSKKQRDCGETARDSLAYSC 82
           ++  S +  T  DRFIPCR+ +              D  P T  K+          + AYS
Sbjct: 35  SSLSSPSKSTCSDRFIPCRSSSRLHAF-----DLQDKEPTTPVKEGG-------NEAYSR 82

Query: 83  LLKNELLGSAIDDV---KTAGEERNENAYTPAAKRSLFKYQSPTKQDYNGECPYSLSPVS 139
           LLK+EL GS            G+    +  +P      FK          +   P  L   +
Sbjct: 83  LLKSELFGSDFASPLLSPAGGQGSASSPMSPCTNMLRFKTDRSNSSPSSPFSPSILGNDN 142

Query: 140 AKSQKLLRSPRKATRKISRIPFKVLDAPELQDDFYLNLVDWSSQNVLAVGLGSCVYLWSA 199
             S      P K  RK+ + P KVLDAP LQDDFYLN+VDWSSQNVLAVGLG+CVYLW+A
Sbjct: 143 GHSSDS-SPPPKPPRKVPKTPHKVLDAPSLQDDFYLNVVDWSSQNVLAVGLGTCVYLWTA 201

Query: 200 CTSQVTRLCDLSPDANTVTSVSWNERGNTVAVGTHHGYVTVWDVAANKQINKLNGHSARV 259
             S+VT+LCDL P+ ++V SV W   G+ +++GT HG V VWD    K++  + GH  R
Sbjct: 202 SNSKVTKLCDLGPN-DSVCSVQWTREGSYISIGTSHGQVQVWDGTQCKRVRTMGGHQTRT 260

Query: 260 GALAWNSDILSSGSRDRWIIQRDTRTPQLQSERRLAGHRQEVCGLKWSPDNQYLASGGND 319
           G LAWNS ILSSGSRDR I+Q D R  Q     +L GH+ EVCGLKWS D++ LASGGND
Sbjct: 261 GVLAWNSRILSSGSRDRNILQHDIRV-QSDFVSKLVGHKSEVCGLKWSHDDRELASGGND 319

Query: 320 NRLYVWNQHSVNPVQSYTEHMAAVKAIAWSPHHHGLLASGGGTADRCIRFWNTLTGQPMQ 379
           N+L VWN HS  P+   TEH AAVKAI WSPH   LLASGGGTADRCIRFWNT  G  +
Sbjct: 320 NQLLVWNNHSQQPILKLTEHTAAVKAITWSPHQSSLLASGGGTADRCIRFWNTTNGNQLN 379

Query: 380 CVDTGSQVCNLAWSKHSSELVSTHGYSQNQILVWKYPSLTQVAKLTGHSYRVLYLALSPD 439
            +DTGSQVCNLAWSK+ +E+VSTHGYSQNQI++WKYPS+++VA LTGHS RVLYLA SPD
Sbjct: 380 SIDTGSQVCNLAWSKNVNEIVSTHGYSQNQIMLWKYPSMSKVATLTGHSMRVLYLATSPD 439

Query: 440 GEAIVTGAGDETLRFWNVFSKARSQ 464
           G+ IVTGAGDETLRFWNVF   + Q
```

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Sbjct: 440 GQTIVTGAGDETLRFWNVFPSVKMQ 464

CPU time:     0.37 user secs.       0.04 sys. secs          0.41 total secs.

Gapped
Lambda      K       H
   0.314    0.129    0.393

Gapped
Lambda      K       H
   0.270   0.0470    0.230


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 2391
Number of Sequences: 0
Number of extensions: 159
Number of successful extensions: 16
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 472
length of database: 181,542,687
effective HSP length: 55
effective length of query: 417
effective length of database: 160,388,367
effective search space: 66881949039
effective search space used: 66881949039
T: 9
A: 40
X1: 16 ( 7.2 bits)
X2: 128 (49.9 bits)
X3: 128 (49.9 bits)
S1: 42 (22.0 bits)
S2: 60 (27.8 bits)
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1: BAB11112. cell cycle switch...[gi:10177650] BLink, Nucleotide, Related Sequences, PubMed, Taxonomy, LinkOut

```
LOCUS       BAB11112                472 aa            linear   PLN 27-DEC-2000
DEFINITION  cell cycle switch protein [Arabidopsis thaliana].
ACCESSION   BAB11112
VERSION     BAB11112.1  GI:10177650
DBSOURCE    locus AB005230 accession AB005230.2
KEYWORDS    .
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Sato,S., Kotani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M.,
            Miyajima,N. and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 5. I.
            Sequence features of the 1.6 Mb regions covered by twenty
            physically assigned P1 clones
  JOURNAL   DNA Res. 4 (3), 215-230 (1997)
  MEDLINE   97471969
   PUBMED   9330910
REFERENCE   2  (residues 1 to 472)
  AUTHORS   Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MAC12
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
            shorter because we remove overlaps between neighboring submissions.
            The 5' clone is MXE10 and the 3' clone is MUA22.
FEATURES             Location/Qualifiers
     source          1..472
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia"
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                     /chromosome="5"
                     /clone="MAC12"
                     /clone_lib="Mitsui P1"
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                     /product="cell cycle switch protein"
     CDS             1..472
                     /coded_by="complement(join(AB005230.2:19277..19435,
                     AB005230.2:19524..19820,AB005230.2:19943..20185,
                     AB005230.2:20272..20376,AB005230.2:20468..20590,
                     AB005230.2:20688..21179))"
                     /note="gene_id:MAC12.21"
ORIGIN
        1 maspqstktg lnlpagmnqt slrletfsss frgisslssp skstcsdrfi pcrsssrlha
       61 fdlqdkeptt pvkeggneay srllkselfg sdfaspllsp aggqgsassp mspctnmlrf
      121 ktdrsnssps spfspsilgn dnghssdssp ppkpprkvpk tphkvldaps lqddfylnvv
      181 dwssqnvlav glgtcvylwt asnskvtklc dlgpndsvcs vqwtregsyi sigtshgqvq
      241 vwdgtqckrv rtmgghqtrt gvlawnsril ssgsrdrnil qhdirvqsdf vsklvghkse
      301 vcglkwshdd relasggndn qllvwnnhsq qpilklteht aavkaitwsp hqssllasgg
      361 gtadrcirfw nttngnqlns idtgsqvcnl awsknvneiv sthgysqnqi mlwkypsmsk
      421 vatltghsmr vlylatspdg qtivtgagde tlrfwnvfps vkmqvcilfs sl
//
```

Revised: October 24, 2001.